

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 24, 2006, 07:58:59 ; Search time 3940 Seconds  
(without alignments)  
1644.709 Million cell updates/sec

Title: US-10-621-741A-1  
Perfect score: 638  
Sequence: 1 KPKEDREWEKFKTKHITSQS.....FICITCRDNYPVHFVKTGKC 114

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10621741/runat\_23022006\_111443\_20635/app\_query.fasta\_1  
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03h  
-USER=US10621741@CGN\_1\_1\_4939@runat\_23022006\_111443\_20635 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_in:  
3: gb\_env:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pr:  
9: gb\_ro:  
10: gb\_sts:  
11: gb\_sy:  
12: gb\_un:  
13: gb\_vi:  
14: gb\_htg:  
15: gb\_pl:

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 24, 2006, 08:00:12 ; Search time 495 Seconds  
(without alignments)  
1534.899 Million cell updates/sec

Title: US-10-621-741A-1  
Perfect score: 638  
Sequence: 1 KPKEDREWEKFKTKHITSQS.....FICITCRDNYPVHFVKTGKC 114

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10621741/runat_23022006_111442_20617/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US10621741@CGN_1_1_727@runat_23022006_111442_20617 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : N\_Geneseq\_21:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 24, 2006, 08:06:59 ; Search time 167 Seconds  
(without alignments)  
1213.425 Million cell updates/sec

Title: US-10-621-741A-1  
Perfect score: 638  
Sequence: 1 KPKEDREWEKFKTKHITSQS.....FICITCRDNYPVHFVKTGKC 114

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10621741/runat\_23022006\_111447\_20725/app\_query.fasta\_1  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss03h -USER=US10621741@CGN\_1\_1\_193@runat\_23022006\_111447\_20725  
-NCPU=6 -ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/1/ina/1\_COMB.seq:  
2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq:  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:  
5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq:  
6: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:  
7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq:  
8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq:  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 24, 2006, 08:32:00 ; Search time 792 Seconds  
(without alignments)  
1190.289 Million cell updates/sec

Title: US-10-621-741A-1  
Perfect score: 638  
Sequence: 1 KPKEDREWEKFKTKHITSQS.....FICITCRDNYPVHFVKTGKC 114

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame\_p2n.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10621741/runat\_23022006\_111454\_20895/app\_query.fasta\_1  
-DB=Published\_Applications\_NA\_Main -QFMT=fastap -SUFFIX=p2n.rnpbm  
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1  
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext  
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p  
-USER=US10621741@CGN\_1\_1\_1549@runat\_23022006\_111454\_20895 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA\_Main:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 24, 2006, 08:43:20 ; Search time 298 Seconds  
(without alignments)  
815.738 Million cell updates/sec

Title: US-10-621-741A-1

Perfect score: 638

Sequence: 1 KPKEDREWEKFKTKHITSQS.....FICITCRDNYPVHFVKTGKC 114

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10621741/runat_23022006_111457_20952/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss08
-USER=US10621741@CGN_1_1_220@runat_23022006_111457_20952 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : Published\_Applications\_NA\_New:\*

```
1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 24, 2006, 08:02:27 ; Search time 3240 Seconds  
(without alignments)  
1646.212 Million cell updates/sec

Title: US-10-621-741A-1  
Perfect score: 638  
Sequence: 1 KPKEDREWEKFKTKHITSQS.....FICITCRDNYPVHFVKTGKC 114

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10621741/runat_23022006_111445_20660/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss07
-USER=US10621741@CGN_1_1_5315@runat_23022006_111445_20660 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database :

```
EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2006, 08:56:31 ; Search time 2414 Seconds  
(without alignments)  
8053.215 Million cell updates/sec

Title: US-10-621-741A-2

Perfect score: 342

Sequence: 1 aaaccgaaagaagaccgtga.....tcgttaaaactggtaaatgc 342

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:\*
1: gb\_ba:\*
2: gb\_in:\*
3: gb\_env:\*
4: gb\_om:\*
5: gb\_ov:\*
6: gb\_pat:\*
7: gb\_ph:\*

8: gb\_pr:\*

9: gb\_ro:\*

10: gb\_sts:\*

11: gb\_sy:\*

12: gb\_un:\*

13: gb\_vi:\*

14: gb\_htg:\*

15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2006, 08:51:26 ; Search time 399 Seconds  
(without alignments)  
5712.594 Million cell updates/sec

Title: US-10-621-741A-2

Perfect score: 342

Sequence: 1 aaaccgaaagaagaccgtga.....tcgttaaaaactggtaatgc 342

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2006, 08:59:04 ; Search time 103 Seconds  
(without alignments)  
5902.195 Million cell updates/sec

Title: US-10-621-741A-2  
Perfect score: 342  
Sequence: 1 aaaccgaaagaagaccgtga.....tcgttaaaactggtaatgc 342

Scoring table: IDENTITY\_NUC  
Gapext 1.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/1\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq:\*

8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq:\*

9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

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## OM nucleic - nucleic search, using sw model

Run on: February 24, 2006, 09:03:52 ; Search time 580 Seconds  
(without alignments)  
4876.082 Million cell updates/sec

Title: US-10-621-741A-2  
Perfect score: 342  
Sequence: 1 aaaccgaaagaagaccgtga.....tcgttaaaactggtaatgc 342

Scoring table: IDENTITY\_NUC  
Gapext 1.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2006, 09:07:35 ; Search time 309 Seconds  
(without alignments)  
2360.095 Million cell updates/sec

Title: US-10-621-741A-2

Perfect score: 342

Sequence: 1 aaaccgaaagaagaccgtga.....tcgttaaaactggtaatgc 342

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_New:\*

1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*

2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*

5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq1:\*

7: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq1:\*

9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*

10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*

11: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq3:\*

12: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq4:\*

13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2006, 08:57:47 ; Search time 3742 Seconds  
(without alignments)  
4276.104 Million cell updates/sec

Title: US-10-621-741A-2

Perfect score: 342

Sequence: 1 aaaccgaaagaagaccgtga.....tcgttaaaactggtaatgc 342

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_htc:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_est7:\*

9: gb\_gss1:\*

10: gb\_gss2:\*

11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.